Package 'boot.heterogeneity'

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Type Package

Title A Bootstrap-Based Heterogeneity Test for Meta-Analysis

Version 0.1.0

Maintainer Ge Jiang <gejiang2@illinois.edu>

Description Implements a bootstrap-based heterogeneity test for standardized mean differences (d), Fisher-transformed Pearson's correlations (r), and natural-logarithm-transformed odds ratio (or) in meta-analysis studies. Depending on the presence of moderators, this Monte Carlo based test can be implemented in the random- or mixed-effects model. This package uses rma() function from the R package 'metafor' to obtain parameter estimates and likelihoods, so installation of R package 'metafor' is required. This approach refers to the studies of Anscombe (1956) <doi:10.2307/2332926>, Haldane (1940) <doi:10.2307/2332614>, Hedges (1981) <doi:10.3102/10769986006002107>, Hedges & Olkin (1985, ISBN:9
0123363800), Silagy, Lancaster, Stead, Mant, & Fowler (2004) <doi:10.1002/14651858.CD000146.pub2>, Viechtbauer (2010) <doi:10.18637/jss.v036.i03>, and Zuckerman (1994, ISBN:978-0521432009).

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URL https://github.com/gabriellajg/boot.heterogeneity/

BugReports https://github.com/gabriellajg/boot.heterogeneity/issues

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Author Ge Jiang [aut, cre], Han Du [aut], Zijun Ke [ctb]

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R topics documented:

`boot.d` *Standardized Mean Differences (d): Bootstrap-Based Heterogeneity Test for Between-study Heterogeneity in Random- or Mixed- Effects Model*

Description

`boot.d` returns the bootstrap-based tests of the residual heterogeneity in random- or mixed- effects model of standardized mean differences (d).

Usage

```
boot.d(
  n1,
  n2,
  est,
  model = "random",
  adjust = FALSE,
  mods = NULL,
  nrep = 10^4,
  p_cut = 0.05,
  boot.include = FALSE,
  parallel = FALSE,
  verbose = FALSE
)
```

Arguments

`n1`	a vector of sample sizes from group 1 in each of the included studies.
`n2`	a vector of sample sizes from group 2 in each of the included studies.
`est`	a vector of unbiased estimates of standardized mean differences.
`model`	choice of random- or mixed- effects models. Can only be set to `"random"`, or `"mixed"`.
`adjust`	if biased estimates (i.e., g values) are provided, `adjust` must be set to `TRUE` to compensate for small sample bias. By default, `adjust` is set to `FALSE`.
`mods`	optional argument to include one or more moderators in the model. `mods` is NULL for random-effects model and a dataframe for mixed-effects model. A single moderator can be given as a vector of length k specifying the values of the moderator. Multiple moderators are specified by giving a matrix with k rows and as many columns as there are moderator variables. See `rma` for more details.

nrep	number of replications used in bootstrap imulations. Default to 10^4.
p_cut	cutoff for p-values, which is the alpha level. Default to 0.05.
boot.include	if true, bootstrap simulation results are included in the output (e.g., bootstrap critical values).
parallel	if true, parallel computing using 2 cores will be performed during bootstrapping stage. Otherwise, for loop is used.
verbose	if true, show the progress of boostrapping.

Details

For standardized mean difference, if the biased estimates (i.e., g values) are provided, adjust=TRUE can be specified to obtain the corresponding unbiased estimates.

This function returns the test statistics as well as their p-value and significances using (1) Q-test, (2) Bootstrap-Based Heterogeneity Test with Maximum Likelihood (ML), and (3) Bootstrap-Based Heterogeneity Test with Restricted Maximum Likelihood (REML).

The results of significances are classified as "sig" or "n.s" based on the cutoff p-value (i.e., alpha level). "sig" means that the between-study heterogeneity is significantly different from zero whereas "n.s" means the between-study heterogeneity is not significantly different from zero. The default alpha level is 0.05.

Value

A dataframe that contains the test statistics ('stat'), p-values ('p_value'), and significances of effect size heterogeneity ("Heterogeneity").

References

Hedges, L. V. (1981). Distribution theory for glass's estimator of effect size and related estimators. Journal of Educational and Behavioral Statistics, 6(2), 107–128.

Hedges, L. V., & Olkin, I. (1985). Statistical methods for meta-analysis. San Diego, CA: Academic Press.

Viechtbauer, W. (2010). Conducting meta-analyses in R with the metafor package. Journal of Statistical Software, 36(3), 1-48. URL: http://www.jstatsoft.org/v36/i03/

Examples

```
# Demo 1: A meta-analysis of 18 studies in which the effect of open versus
# traditional education on students' self-concept was studied (Hedges & Olkin, 1985).

selfconcept <- boot.heterogeneity:::selfconcept

# n1 and n2 are lists of samples sizes in two groups
n1 <- selfconcept$n1
n2 <- selfconcept$n2

# g is a list of biased estimates of standardized mean differences in the meta-analytical study
g <- selfconcept$g
cm <- (1-3/(4*(n1+n2-2)-1)) #correct factor to compensate for small sample bias (Hedges, 1981)
```

```
d <- cm*g


boot.run <- boot.d(n1, n2, est = d, model = 'random', p_cut = 0.05)
# is equivalent to:
boot.run2 <- boot.d(n1, n2, est = g, model = 'random', adjust = TRUE, p_cut = 0.05)


# Demo 2: A hypothetical meta-analysis of 15 studies with 3 moderators.
hypo_moder <- boot.heterogeneity:::hypo_moder

boot.run3 <- boot.d(n1 = hypo_moder$n1, n2 = hypo_moder$n2, est = hypo_moder$d, model = 'mixed',
mods = cbind(hypo_moder$cov.z1, hypo_moder$cov.z2, hypo_moder$cov.z3), p_cut = 0.05)


# Note: this boot.d function is supposed to replace its
# earlier version in \link[mc.heterogeneity]{mc.d}.
```

`boot.fcor` *Fisher-transformed Pearson's correlation: Bootstrap-Based Heterogeneity Test for Between-study Heterogeneity in Random- or Mixed-Effects Model*

Description

`boot.fcor` returns the bootstrap-based tests of the residual heterogeneity in random- or mixed-effects model of Pearson's correlation coefficients transformed with Fisher's r-to-z transformation (z scores).

Usage

```
boot.fcor(
  n,
  z,
  model = "random",
  mods = NULL,
  nrep = 10^4,
  p_cut = 0.05,
  boot.include = FALSE,
  parallel = FALSE,
  verbose = FALSE
)
```

Arguments

`n`	a vector of sample sizes in each of the included studies.
`z`	a vector of Fisher-transformed Pearson's correlations.

model	choice of random- or mixed- effects models. Can only be set to "random", or "mixed".
mods	optional argument to include one or more moderators in the model. mods is NULL for random-effects model and a dataframe for mixed-effects model. A single moderator can be given as a vector of length k specifying the values of the moderator. Multiple moderators are specified by giving a matrix with k rows and as many columns as there are moderator variables. See rma for more details.
nrep	number of replications used in bootstrap simulations. Default to 10^4.
p_cut	cutoff for p-values, which is the alpha level. Default to 0.05.
boot.include	if true, bootstrap simulation results are included in the output (e.g., bootstrap critical values).
parallel	if true, parallel computing using 2 cores will be performed during bootstrapping stage. Otherwise, for loop is used.
verbose	if true, show the progress of boostrapping.

Details

This function returns the test statistics as well as their p-value and significances using (1) Q-test, (2) Bootstrap-Based Heterogeneity Test with Maximum Likelihood (ML), and (3) Bootstrap-Based Heterogeneity Test with Restricted Maximum Likelihood (REML).

The results of significances are classified as "sig" or "n.s" based on the cutoff p-value (i.e., alpha level). "sig" means that the between-study heterogeneity is significantly different from zero whereas "n.s" means the between-study heterogeneity is not significantly different from zero. The default alpha level is 0.05.

Value

A dataframe that contains the test statistics ('stat'), p-values ('p_value'), and significances of effect size heterogeneity ("Heterogeneity").

References

Zuckerman, M. (1994). Behavioral expressions and biosocial bases of sensation seeking. New York, NY: Cambridge University Press.

Viechtbauer, W. (2010). Conducting meta-analyses in R with the metafor package. Journal of Statistical Software, 36(3), 1-48. URL: http://www.jstatsoft.org/v36/i03/

Examples

```
# A meta-analysis of 13 studies studying the correlation
# between sensation seeking scores and levels of monoamine oxidase (Zuckerman, 1994).

sensation <- boot.heterogeneity:::sensation

# n is a list of samples sizes
n <- sensation$n

# Pearson's correlation
```

```
r <- sensation$r

# Fisher's Transformation
z <- 1/2*log((1+r)/(1-r))


#' boot.run <- boot.fcor(n, z, model = 'random', p_cut = 0.05)

# Note: this boot.fcor function is supposed to replace its
# earlier version in \link[mc.heterogeneity]{mc.fcor}.
```

`boot.lnOR` *Natural-Logarithm-Transformed Odds Ratio (lnOR): Bootstrap-Based Heterogeneity Test for Between-study Heterogeneity in Random- or Mixed- Effects Model*

Description

`boot.lnOR` returns the bootstrap-based tests of the residual heterogeneity in random- or mixed-effects model of natural-logarithm-transformed observed odds ratio (lnOR).

Usage

```
boot.lnOR(
  n_00,
  n_01,
  n_10,
  n_11,
  model = "random",
  mods = NULL,
  nrep = 10^4,
  p_cut = 0.05,
  boot.include = FALSE,
  parallel = FALSE,
  verbose = FALSE
)
```

Arguments

`n_00`	a vector of number of participants who score negatively on both Y1 and Y2 (e.g., mortality cases in the control group).
`n_01`	a vector of number of participants who score negatively on Y1 and positively on Y2 (e.g., recovery cases in the control group).
`n_10`	a vector of number of participants who score positively on Y1 and negatively on Y2 (e.g., mortality cases in the experimental group).
`n_11`	a vector of number of participants who score positively on both Y1 and Y2 (e.g., recovery cases in the experimental group).

model	choice of random- or mixed- effects models. Can only be set to "random", or "mixed".
mods	optional argument to include one or more moderators in the model. mods is NULL for random-effects model and a dataframe for mixed-effects model. A single moderator can be given as a vector of length k specifying the values of the moderator. Multiple moderators are specified by giving a matrix with k rows and as many columns as there are moderator variables. See rma for more details.
nrep	number of replications used in bootstrap simulations. Default to 10^4.
p_cut	cutoff for p-values, which is the alpha level. Default to 0.05.
boot.include	if true, bootstrap simulation results are included in the output (e.g., bootstrap critical values).
parallel	if true, parallel computing using 2 cores will be performed during bootstrapping stage. Otherwise, for loop is used.
verbose	if true, show the progress of boostrapping.
lnOR	a vector of natural-logarithm-transformed odds ratio in the included studies, which is calculated as ln(n11*n00/n01/n10)

Details

For odds ratio, its standard error will be infinite if any one of the four cells in the contingency tables is zero. In this case, Haldane and Anscombe correction is used by adding 0.5 to each cell value (Anscombe, 1956; Haldane, 1940). This function returns the test statistics as well as their p-value and significances using (1) Q-test, (2) Bootstrap-Based Heterogeneity Test with Maximum Likelihood (ML), and (3) Bootstrap-Based Heterogeneity Test with Restricted Maximum Likelihood (REML).

The results of significances are classified as "sig" or "n.s" based on the cutoff p-value (i.e., alpha level). "sig" means that the between-study heterogeneity is significantly different from zero whereas "n.s" means the between-study heterogeneity is not significantly different from zero. The default alpha level is 0.05.

Value

A dataframe that contains the test statistics ('stat'), p-values ('p_value'), and significances of effect size heterogeneity ("Heterogeneity").

Source

Silagy C, Lancaster T, Stead LF, Mant D, Fowler G. (2004). Nicotine replacement therapy for smoking cessation. Cochrane Database of Systematic Reviews 2004, Issue 3. Art. No.: CD000146. DOI: 10.1002/14651858.CD000146.pub2.

References

Anscombe, F. J. (1956). On estimating binomial response relations. Biometrika, 43(3/4), 461–464.

Haldane, J. (1940). The mean and variance ofl chi 2, when used as a test of homogeneity, when expectations are small. Biometrika, 31(3/4), 346–355.

Viechtbauer, W. (2010). Conducting meta-analyses in R with the metafor package. Journal of Statistical Software, 36(3), 1-48. URL: http://www.jstatsoft.org/v36/i03/

Examples

```
# A meta-analysis consists of 26 studies on nicotine replacement therapy for smoking cessation
library(HSAUR2)
data(smoking)

# Y1: receive treatment; Y2: stop smoking
n_00 <- smoking$tc - smoking$qc  # not receive treatement yet not stop smoking
n_01 <- smoking$qc # not receive treatement but stop smoking
n_10 <- smoking$tt - smoking$qt # receive treatement but not stop smoking
n_11 <- smoking$qt # receive treatement and stop smoking
lnOR <- log(n_11*n_00/n_01/n_10)


boot.run <- boot.lnOR(n_00, n_01, n_10, n_11, model = 'random', p_cut = 0.05)

# Note: this boot.lnOR function is supposed to replace
# its earlier version in \link[mc.heterogeneity]{mc.lnOR}.
```

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